

circumference to mature trees, were observed in all areas visited. Further studies, of sites specifically mentioned in previous reports, are necessary to confirm the possibly role of fungal disease on the decline of natural populations of *A. dichotoma* trees.

doi:[10.1016/j.sajb.2009.02.100](https://doi.org/10.1016/j.sajb.2009.02.100)

### Phytocystatins: A comparative analysis of cysteine protease inhibitors in plants

U. Schlüter<sup>a</sup>, B.J. Vorster<sup>a</sup>, Ö. Tastan Bishop<sup>b</sup>, K.J. Kunert<sup>a</sup>, D. Michaud<sup>c</sup>

<sup>a</sup>Department of Plant Science, University of Pretoria, Pretoria 0002, South Africa

<sup>b</sup>Bioinformatics and Computational Biology Unit, Department of Biochemistry, University of Pretoria, Pretoria 0002, South Africa

<sup>c</sup>Département de Phytologie, Université Laval, Quebec City (QC), Canada G1V 0A6

Phytocystatins are inhibitors of papain like cysteine proteases. In plants, their activity is associated with the regulation of developmental processes, and with responses to abiotic and biotic stresses. Since many plant pests also rely on cysteine proteases for the breakdown of plant proteins, cystatins can reduce the accessibility of plant resources for the invader. Up to now, research has therefore focussed on the use of phytocystatins as pest control agents, and much less is known about their specific endogenous function in plants. Differences in the expression patterns and the primary amino acid sequence of these proteins indicate more specialised functions for some phytocystatins. A comparison of 153 phytocystatin encoding sequences showed high sequence homology in the reactive site of the second loop, but amino acid substitutions in these consensus motifs does not necessarily lead to inactivation of the protein. Phytocystatins from rice (OCI) and papaya, for instance, show considerable differences in the consensus motifs, and the importance of specific amino acids in the active site will now be tested by site-directed mutagenesis. Structural models for these two cystatins will be created and assessed for their potential interaction with different proteases.

doi:[10.1016/j.sajb.2009.02.101](https://doi.org/10.1016/j.sajb.2009.02.101)

### A systematic appraisal of the taxonomic limits of the *C. brachiata* complex

K. Singh<sup>a</sup>, K. Balkwill<sup>b</sup>, R.A. Reddy<sup>b</sup>

<sup>a</sup>South African National Biodiversity Institute, Private Bag X7, Claremont 7735, South Africa

<sup>b</sup>School of Animal, Plant and Environmental Sciences, University of Witwatersrand, Private Bag 3, WITS 2050, South Africa

*Clematis brachiata* Thunb., *C. stewartiae* Burtt Davy and *C. oweniae* Harv. are each known to be highly variable morphologically and have a large degree of morphological overlap in various descriptions. Furthermore, there is some indication of changes in diagnostic characters occurring within a single the growing season in *C. brachiata*. As a result it is difficult to determine where the taxonomic distinctness for these species lies or if it even exists. The validity of these three taxa were tested using a numerical approach. First a population was monitored to determine if there are any changes in diagnostic characters over a single flowering/fruiting season. These specimens were combined with specimens from across southern Africa to determine if these changes have any impact on the complex as a whole. Known hybrid specimens with *C. villosa* ssp. *stanleyi* were later added to determine if hybridization has any effect on the taxonomic limits observed. Ordination (principal co-ordinates analysis) and clustering analysis (Unweighted Pair Group Method of Arithmetic Averages) algorithms in NTSys-pc 2.2 were used to identify any discrete groups and the characters that define those groups. *C. villosa* ssp. *stanleyi* was used as a calibrating species. No significant changes were found in the diagnostic characters across a single flowering/fruiting season. When added to the greater southern African specimens it was revealed that there is only one species within the “*Clematis brachiata* complex” with a high amount of morphological variation. The name recognized for the complex is *Clematis brachiata* and the names *C. oweniae* Harv. and *C. stewartiae* are thus synonyms. The inclusion of the hybrid specimens revealed that hybridization does influence morphology observed, the extent of which needs to be investigated further.

doi:[10.1016/j.sajb.2009.02.102](https://doi.org/10.1016/j.sajb.2009.02.102)

### Variation in leaf traits and their effects in physiological processes in *Leucospermum conocarpodendron*

R.P. Skelton<sup>a</sup>, J.J. Midgley<sup>a</sup>, S.D. Johnson<sup>b</sup>, M.D. Cramer<sup>a</sup>

<sup>a</sup>Department of Botany, University of Cape Town, Rondebosch 7700, South Africa

<sup>b</sup>School of Biological and Conservation Sciences, University of KwaZulu-Natal Pietermaritzburg, Private Bag X01, Scottsville 3209, South Africa

*Leucospermum conocarpodendron* displays considerable variation in leaf traits across its biogeographical range. The variation in leaf traits such as leaf hairiness, stomatal density, specific leaf area and leaf size, as well as  $\delta^{13}\text{C}$  (as an indication of intrinsic water use efficiency) were quantified. The differences in environmental conditions that may have selected for diverse traits were analysed. Plants with hairy leaves had greater stomatal density ( $t=-19.8$ , d.f.=118;  $p<0.05$ ), smaller leaf area ( $t=5.5$ ; d.f.=98;  $p<0.05$ ) and higher  $\delta^{15}\text{N}$  values ( $t=-5.5$ ; d.f.=118;  $p<0.05$ ) than those with glabrous leaves. No significant difference in  $\delta^{13}\text{C}$  or SLA was found. Hairy leaves had